

#30  
1/2/01  
1644  
HFL

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/08/756,018C  
 DATE: 01/02/2001  
 TIME: 10:20:46

**ENTERED**

Input Set : A:\ES.txt  
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4 <110> APPLICANT: Brian Seed  
 5 Tara Pouyani  
 7 <120> TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES  
 8 AND METHODS  
 10 <130> FILE REFERENCE: 00786/284002  
 12 <140> CURRENT APPLICATION NUMBER: 08/756,018C  
 13 <141> CURRENT FILING DATE: 1996-11-25  
 15 <150> PRIOR APPLICATION NUMBER: 60/000,213  
 16 <151> PRIOR FILING DATE: 1995-06-14  
 18 <150> PRIOR APPLICATION NUMBER: 08/661,960  
 19 <151> PRIOR FILING DATE: 1996-06-12  
 21 <160> NUMBER OF SEQ ID NOS: 17  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 26 <211> LENGTH: 10  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Homo sapiens  
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 32 1 5 10  
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 36 <211> LENGTH: 18  
 37 <212> TYPE: PRT  
 38 <213> ORGANISM: Homo sapiens  
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 42 1 5 10 15  
 43 Val Thr  
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 48 <211> LENGTH: 42  
 49 <212> TYPE: PRT  
 50 <213> ORGANISM: Homo sapiens  
 52 <400> SEQUENCE: 3  
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 54 1 5 10 15  
 55 Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp  
 56 20 25 30  
 57 Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro  
 58 35 40  
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 62 <211> LENGTH: 20  
 63 <212> TYPE: PRT  
 64 <213> ORGANISM: Homo sapiens  
 66 <400> SEQUENCE: 4  
 67 Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe  
 68 1 5 10 15  
 69 Leu Pro Glu Thr

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75 <212> TYPE: PRT
76 <213> ORGANISM: Homo sapiens
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81 Leu Pro Glu Thr
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86 <211> LENGTH: 20
87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
90 <400> SEQUENCE: 6
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92 1          5          10          15
93 Leu Pro Glu Ala
94          20
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 20
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
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104 1          5          10          15
105 Leu Pro Glu Ala
106          20
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111 <212> TYPE: DNA
112 <213> ORGANISM: Homo sapiens
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116 gglgtccagt ccaggtgca gclgggtgcag tctggggctg aggtgaagaa gctggggctc      120
117 tcggtgaagg tctcctgcaa ggetttctgga qgcacettca gcaqctatgc tatcagctgg      180
118 gtgcgacagg ccctggaca aggtcttgag tggatgggag ggatcctccc tatctttggt      240
119 acagcaaaact acgcacagaa gtccagggc agagtcacga ttaccgcgga cgaatccacg      300
120 aqcacagcct acatggagct gacagcctg agatctgagg acacggcctg gtattactgt      360
121 gcgagagata atggagcgtt ttgtagtggt ggtagctgct actcggtctg gttcgacccc      420
122 tggggccagg gaacctgggt caccgtctct tcaggtgagt actgaattct agctttctgg      480
123 ggcaggccag gctgacctt ggetttgggg cagggagggg gctaagggtg ggcagggtgg      540
124 gccagcagg gtacacccaa tgcctatgag cccagacact ggaagctgaa cctcgcgga      600
125 agttaagaac ccggggcct ctgcgcctgg gccagctctt gtcacacacc ggggtcacat      660
126 ggcaccacct ctctgcagc ctccaccaag ggcacatcgg tcttccctcc ggcacctcc      720
127 tccaagagca cctctggggg cacagcgccc ctgggtgccc tggtraaggc ctacttccc      780
128 gaaccggtga cgtgtcgtg gaactcaggg gccctgacca gcggcggtga caacttccc      840
129 gctgtcctac agtctcagg actctactcc ctccagcagc tgggtaccgt gccctccagg      900
130 agcttgggca cccagacctt catctgcaac gtgaatcaca ayccacagca ccccaagglt      960

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131 gacaaagaaag ttggtgagag gccagcacag ggaaggaggg tgtctgtctg agcaagctc 1020
132 agcgtctctg cctggagcga tcccggtat gcagcccccag tccagggcag caaggcagge 1080
133 cccgtctctg ccttcacccg gaggctctgc ccccccact catgtctcag gagaaggtct 1140
134 tctggtttt tcccagctc tgggcagcga caggctaggt gccctaaccc caagccctcc 1200
135 acacaaaggg gcaggtgctg ggtcagacc tcccaagagc cctatccggg aggaacctgc 1260
136 cctgacctc agcccccacc aaaggccaaa ctctccactc cctcagctcg gacaccttct 1320
137 cctctccacg attcagtaa ctcccactct tctctctgca gaggcccaat cttgtgacaa 1380
138 aactcacaca tgcacacctt gcccaagtaa gccagccag gctcagccct ccaactcaag 1440
139 ggcggagcag tgcctagag tagctgcat ccaggacag gccccagccg ggtgctgaca 1500
140 cgtccacctc cactctctc tcagcactg aactccctgg gggacccgca gcttctctct 1560
141 tccccccaaa acccaaggac acctcctga tctcccgac cctgaggtc acatgcgttg 1620
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143 aggtgcataa tgcacagaca aagccgcggg agagcagta caacagcag faaccgggtg 1740
144 tcagctctct caccctctc caccaggact ggtgaaatg caaggagtac aagtgcacag 1800
145 tctccacaaa agcctctcca gccccctcag agaaaacct ctccaaagcc aaagggtgga 1860
146 cccgtgggtt gcagagcga catgacaga gcccggtcag gccaccctc tgcctgaga 1920
147 gtgacgctg taccaacctc tgtctacag gccagcccg agaacccag gtgtacccc 1980
148 tgcctccatc ccgggatyag ctgaccaaga accaggtcag cctgacctgc ctggtcaag 2040
149 gcttctatcc cagcagctc gccgtgagt gggagaccaa tggcagccg gagacaaact 2100
150 acaagaccac gctcccgct ctgactccg accgtctctt ctctctctac agcaagctca 2160
151 cgtgacaaa gacaggtg cagcagcga acgtctctc atgtctcgt atgcatgag 2220
152 ctctgcacaa ccactacag caaagagcc tctccctgic tccgggttaa tgggtgag 2280
153 ggcgggc 2287

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156 <211> LENGTH: 442
157 <212> TYPE: PRF
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163 Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly
164 20 25 30
165 Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
166 35 40 45
167 Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala
168 50 55 60
169 Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly
170 65 70 75 80
171 Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala
172 85 90 95
173 Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser
174 100 105 110
175 Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
176 115 120 125
177 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
178 130 135 140
179 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
180 145 150 155 160
181 Lys Asp Thr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala

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182	165	170	175
183 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly			
184	180	185	190
185 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Asp Lys			
186	195	200	205
187 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys			
188	210	215	220
189 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro			
190 225	230	235	240
191 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys			
192	245	250	255
193 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp			
194	260	265	270
195 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu			
196	275	280	285
197 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu			
198	290	295	300
199 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn			
200 305	310	315	320
201 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly			
202	325	330	335
203 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu			
204	340	345	350
205 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr			
206	355	360	365
207 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn			
208	370	375	380
209 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe			
210 385	390	395	400
211 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn			
212	405	410	415
213 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr			
214	420	425	430
215 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
216	435	440	
219 <210> SEQ ID NO: 10			
220 <211> LENGTH: 1894			
221 <212> TYPE: DNA			
222 <213> ORGANISM: Homo sapiens			
224 <400> SEQUENCE: 10			
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226 ccattgtgtg ccaacctagt accggtgcc atcaccacag ccacctggga ccagatcact	120		
227 ggcaagtggg ttatatatgc atcgcccttt cgaacagagg agtacaataa gtcgggttcag	180		
228 gagatccaag caaccttctt ttacttcacc cccaacaaga cagaggacac gatctttctc	240		
229 agagagtacc agaccagaca ggaccagtgc atctataaca ccacctacct gaatgtccag	300		
230 cgggaaaatg ggaacctctc cagatacgtg ggaggccaag agcatttcgc tcaattgctg	360		
231 atcttcaggg acaccaagac ctacatgctt gcttttgacg tgaacgatga gaagaactgg	420		
232 gggctgtctg tctatgctga caagccagag acgaccaagg agcaactggg agagttctac	480		
233 gaagctctcg actgcttgcg ccttcccaag tcagatgtcg tglacaccga ttggaaaaag	540		

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234 qataagtggtg agccactgga gaagcagcac gagaaggaga ggaacacgga ggagggggaa      600
235 tgggataccg aggggtgagta ctangcttea gcgctcctgc ctggacgcat ccggctatg      660
236 caqcccaqgl ccaqggcagc aagqcaagcc ccgtctgctt ctccaccggg agcctctgoc      720
237 cgccecactc atgctcaagg agagggcttt ctgctttttt cccaggtctt ggcacagcac      780
238 aggtctaggtg cccctaaccg aggcctgca cacaaggggg caggtgctgg gctcagacct      840
239 gccaaagacc atalcgggga ggacctgccc ctgacctaa gccacaccca aagcccaaac      900
240 tctccactcc ctacgtctcg acacctcttc tctcccaaga tccagtaac tcccaatctt      960
241 ctctctgcag agcccaaatc ttgtgacaaa actcacacat gccacacgtg cccaggttaag     1020
242 ccagcccaqg cctcgccctc cagctcaagg cgggacaggt gccctagagt agcctgcctc     1080
243 cagggacagq cccacggcgg gtgctgacac gtccacctcc atctcttctt cagcaacta     1140
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245 ctcccgacc cctgaggtca catgctggtt ggtggacgtg agccacgaaq accctgaggt     1260
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255 cgtctctctc tgcctcgtga tgcctgaggc tctgcacaa cactacacgc agaagagcct     1860
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267 20 25 30
268 Asn Ala Thr Leu Asp Gln Ile Thr Gly Lys Trp Phe Tyr Ile Ala Ser
269 35 40 45
270 Ala Phe Arg Asn Glu Glu Tyr Asn Lys Ser Val Gln Glu Ile Gln Ala
271 50 55 60
272 Thr Phe Phe Tyr Phe Thr Pro Asn Lys Thr Glu Asp Thr Ile Phe Leu
273 65 70 75 80
274 Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile Tyr Asn Thr Thr Tyr
275 85 90 95
276 Leu Asn Val Gln Arg Glu Asn Gly Thr Ile Ser Arg Tyr Val Gly Gly
277 100 105 110
278 Gln Glu His Phe Ala His Leu Leu Ile Leu Arg Asp Thr Lys Thr Tyr
279 115 120 125
280 Met Leu Ala Phe Asp Val Asn Asp Glu Lys Asn Trp Gly Leu Ser Val
281 130 135 140
282 Tyr Ala Asp Lys Pro Glu Thr Thr Lys Glu Gln Leu Gly Glu Phe Tyr
283 145 150 155 160
284 Glu Ala Leu Asp Cys Leu Arg Ile Pro Lys Ser Asp Val Val Tyr Thr

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VERIFICATION SUMMARY

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